

***Myxochlamys* (Zingiberaceae), a new genus from Borneo**

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A new genus and species, *Myxochlamys mullerensis* (Zingiberaceae) from Central Kalimantan, Borneo is described. This new species is characterized by indistinct pseudostems; congested inflorescences with spirally arranged bracts; copious, highly viscous, axillary-pooled mucus secreted from glands on imbricate bracts; and flowers with a concave labellum, versatile anthers, and a groove formed by the inner surface of the corolla tube to envelope and hold the style. Parallel orientation of the plane of distichy of the leafy shoots, well-developed staminodes, and labellum not connate with the filament suggest that *Myxochlamys* belongs to the tribe Zingibereae. Among the genera in Zingibereae, *Myxochlamys* is similar to *Scaphochlamys* in that it lacks a distinct pseudostem and spiral inflorescence; it is distinct from *Scaphochlamys*, however, in that it has a groove within the corolla tube, concave labellum and versatile anthers. Phylogenetic analyses based on DNA sequences of the nuclear internal transcribed spacer (ITS) and maturase K (*matK*) of the chloroplast DNA show similarity with *Distichochlamys*, *Myxochlamys*, and *Scaphochlamys*. The similarities and differences between *Myxochlamys* and related genera are discussed.

Key words: Borneo, *Myxochlamys*, *Myxochlamys mullerensis*, molecular phylogeny, new genus, *Scaphochlamys*, Zingiberaceae, Zingibereae

The Zingiberaceae comprise a pantropical family of 53 genera and over 1200 species (Kress *et al.* 2002) with a center of diversity is southern and southeastern Asia (Larsen *et al.* 1998). Traditionally, four tribes (Alpinieae Meisn., Globbeae Meisn., Hedychieae Petersen, and Zingibereae Burt & Olatunji) have been recognized in the family based on floral and vegetative characters (Dahlgren *et al.* 1985; Larsen *et al.* 1998). Kress *et al.* (2002) recently proposed a new classification of the Zingiberaceae based on a molecular phylogenetic analysis. They recognized four subfamilies: Siphonochiloideae W. J. Kress (containing only *Siphonochilus*), Tamijioideae W. J. Kress (containing only *Tamijia*), Alpinioideae Link (containing most of the former

Alpinieae), and Zingiberoideae Haask. (containing the remaining genera). Current studies on the molecular phylogenies of the Alpinioideae and some large genera such as *Alpinia*, *Amomum*, and *Etlingera* (Pedersen 2004, Xia *et al.* 2004, Kress *et al.* 2005) suggest that the Zingiberaceae are monophyletic, but require redefined generic boundaries, especially for *Alpinia* and *Amomum*, which are apparently polyphyletic. In Zingiberoideae, Williams *et al.* (2004) showed that Globbeae are monophyletic and sister to Zingibereae; however, the generic limits in the Zingibereae remain unresolved.

In 2004, we explored Muller Range, Central Kalimantan, Indonesia and found an interesting ginger. Parallel orientation of the plane of distichy of

the leafy shoots, well-developed staminodes, and labellum not connate to the filament suggest that the plant belongs to the tribe Zingibereae, but comparative morphological and molecular phylogenetic studies provide evidence against the placement of this plant within any of genera in this tribe. Thus, a new genus, *Myxochlamys*, and new species, *M. mullerensis*, is described here. In accordance with Article 42 of the International Code of Botanical Nomenclature (McNeill *et al.* 2006), the names of the new genus and species are simultaneously validated using the description provided below.

Materials and Methods

Description of the species

The species description is based on studies of plants in the field and in the herbaria of BO, E, HYO, K, and KYO. The plant material studied includes pressed and dried specimens, spirit-fixed floral material, and silica-gel dried tissue for molecular phylogenetic analysis.

Phylogenetic analysis using DNA sequence data

For the DNA analysis, we used nuclear ribosomal DNA of the internal transcribed spacer regions (ITSs; ITS1, 5.8S, and ITS2) and maturase K (*matK*) of the chloroplast DNA. The ITS and *matK* sequences in *Myxochlamys* were generated by the following method and deposited in the DNA Data Bank of Japan (DDBJ). The sequences of other taxa were obtained from GenBank (Appendix 1). Total genomic DNAs were extracted from silica-dried tissues by using the modified CTAB method (Doyle & Doyle 1987, Takano & Okada 2002). ITS sequences were amplified using the ITS5P and ITS8P primers (Möller & Cronk 1997). The chloroplast *matK* region was amplified using *trnK1F* (Manos & Steele 1997) and *trnK2621* (Liston & Kadereit 1995). All amplifications were performed using TaKaRa Ex TaqTM (Takara Bio Inc., Otsu, Shiga, Japan), at annealing temperatures of 50° to

54°C. Amplified products were purified using Microspin S-300 HR columns (Amersham Biosciences, Buckinghamshire, England, UK). Sequencing was performed using ABI PrismTM Big Dye Terminator Cycle Sequencing Ready Reaction Kit (Applied Biosystems, Foster City, California, USA). Sequencing primers included the amplification primers as well as ITS2K (Rangsiruji *et al.* 2000) and ITS3P (Möller & Cronk 1997) for the ITS region and m5R, mSP2R, m5fa, m8R, *matK8R* (all from Kress *et al.* 2002), *matK8* (Steele & Vilgalys 1994), and TA05R (Takano & Okada 2002) for the *matK* region. The products were cleaned using the manufacturer's protocol, and were run on an ABI PrismTM 310 Genetic Analyzer (Applied Biosystems Japan, Tokyo, Japan). Raw sequences were assembled and edited using the BioEdit ver. 5.0.9 software (Hall 1999). DNA sequences were aligned by multiple alignments using the CLUSTALW1.83 computer software package with default settings (Thompson *et al.* 1994).

Phylogenetic analyses

The ITS dataset was analyzed both separately and in combination with the *matK* dataset. To test data incongruence, the incongruence length difference (ILD) test (Farris *et al.* 1995) was implemented as the partition homogeneity test option in PAUP* with 100 replicates for each of two partitions.

Maximum parsimony (MP) was analyzed using PAUP* ver. 4.0. beta 10 (Swofford 2003). Heuristic searches were conducted with SIMPLE addition, tree bisection-reconnection (TBR) branch swapping, and the MULPARS options. Only base substitutions were treated as characters for phylogeny reconstruction. All the gaps were treated as missing values. Support for branches was estimated using bootstrap analysis with 1000 replications (Felsenstein 1985) by a heuristic search using SIMPLE addition, NNT branch swapping, and the MULPARS options. Three species of *Siphonochilus*

were selected as the outgroup (Kress *et al.* 2002).

A Bayesian analysis was conducted using MrBayes v. 3.1.2 (Huelsenbeck & Rohnquist 2001, Rohnquist & Huelsenbeck 2003). The best fitting substitution model for Bayesian analysis was selected using a series of likelihood ratio tests as implemented in Modeltest v. 3.7 (Posada & Crandall 1998). We ran over one million generations of four simultaneous (one cold, three heated) Markov chains by using MrBayes v. 3.1.2 until the average standard deviation of split frequencies (ASDSF) became less than 0.005. The tree from every 100th generation was retained (excluding a quarter of 100/total generations), and a 50% majority rule consensus tree was constructed from these. For each ITS and the combined dataset, the log stabilized before 50 million generations in the Bayesian analysis (1,000,000 for the ITS dataset and 4,500,000 for the combined dataset). The results of the Bayesian analyses are reported as the posterior probabilities (PP; Huelsenbeck & Rohnquist 2001), which are equal to the percentage of trees sampled when a given clade is resolved. Only PP scores excess of 50% are shown in our trees.

The result of exploratory analyses (not shown) that excluded difficult-to-align regions (ITS, 117 pairs) produced more resolved topologies; therefore, in this paper, we present only results from the analyses of the data set excluding ambiguous alignment regions within the ITSs.

Results

Myxochlamys mullerensis A. Takano & Nagam. gen. et sp. nov. (Figs. 1, 2)

Herba rhizomatosa; folia disticha parallela ad rhizoma. Inflorescentia in surculo foliato terminalis, e basi ad apicem florens; bracteae spiraliter dispositae, florem singularem subtendens, mucum gelatinum copiosum secernentes; bracteolae bracteis oppositae, bicarinatae, ad basin apertae. Flores corollae tubo et filamento intra profunde sulcato, stylo per longitudinem in sulco involuto; labellum concavum; anthera versatilis calcaribus basalibus

duobus; ovarium uniloculare, placentatione basali.

Typus. INDONESIA, Central Kalimantan, Murung Raya District, behind Tumbang Naan (0°09'03"S, 113°45'04"E) en route from Sungai (River) Lapangan, a branch of Sungai Joloi (0°11'00"N 113°31'59"E), ca. 200 m from Muara Sopan (0°12'22"N 113°31'23"E), December 21, 2004, H. Okada, H. Nagamasu, H. Tsukaya, A. Takano, & A. Naiki, KT-671 (Holo- BO; iso-HYO, KYO).

Rhizomatous herbs. Rhizome slender, elongate. Leafy shoots close together. Leaves sessile, 3-9, distichous. Plane of leaves parallel to rhizome. Leaf sheath open to the base, 17.5 cm long, ca. 1 cm wide; ligule, 5 mm long. Leaf blades narrowly obovate, to 50 cm long, ca. 7 cm wide, base cuneate, apex acute, upper surface sparsely hairy, uniformly glandular; lower surface densely hairy, uniformly glandular. Inflorescence terminal on a leafy shoot, 4-15 cm long, flowering from the base to apex; scape 2.5-4 cm long. Bracts spirally arranged, imbricate, ca. 5 cm long, ca. 1.3 cm wide, concave, uniformly puberulous, with many glands, blood red, filled with colorless, transparent mucilage. Bracteoles 2-keeled, opposite to bracts, ca. 3.5 cm long, ca. 1.3 cm wide, glabrous, open to base. Flowers solitary. Calyx tubular, ca. 2.5 cm long, split along one side to base, apex with 2 or 3 unequal teeth, glabrous. Corolla tube ca. 4.7 cm long, thick, with a groove formed by inner surface enveloping style; lateral petals ovate, white with red apex, ca. 2 cm long, ca. 0.8 cm wide, slightly hooded; dorsal petal ovate, ca. 2.1 cm long, ca. 0.9 cm wide, slightly hooded, beaked, totally glabrous. Labellum ca. 2.8 cm long, ca. 1.5 cm wide, concave, white with pinkish margin. Lateral staminodes obovate, ca. 5 mm long, ca. 3 mm wide, white. Anther white; filament ca. 5 mm long, with a groove connected to corolla tube and enveloping style; thecae versatile; spur ca. 6 mm long. Ovary ca. 5 mm long, glabrous, unilocular, placentation basal, rudimentary septa present as longitudinal ridges inside ovary. Epigynous glands 4-5 mm long, bilobed. Style white. Stigma white, cup shaped, ciliate around mouth. Fruit unknown.

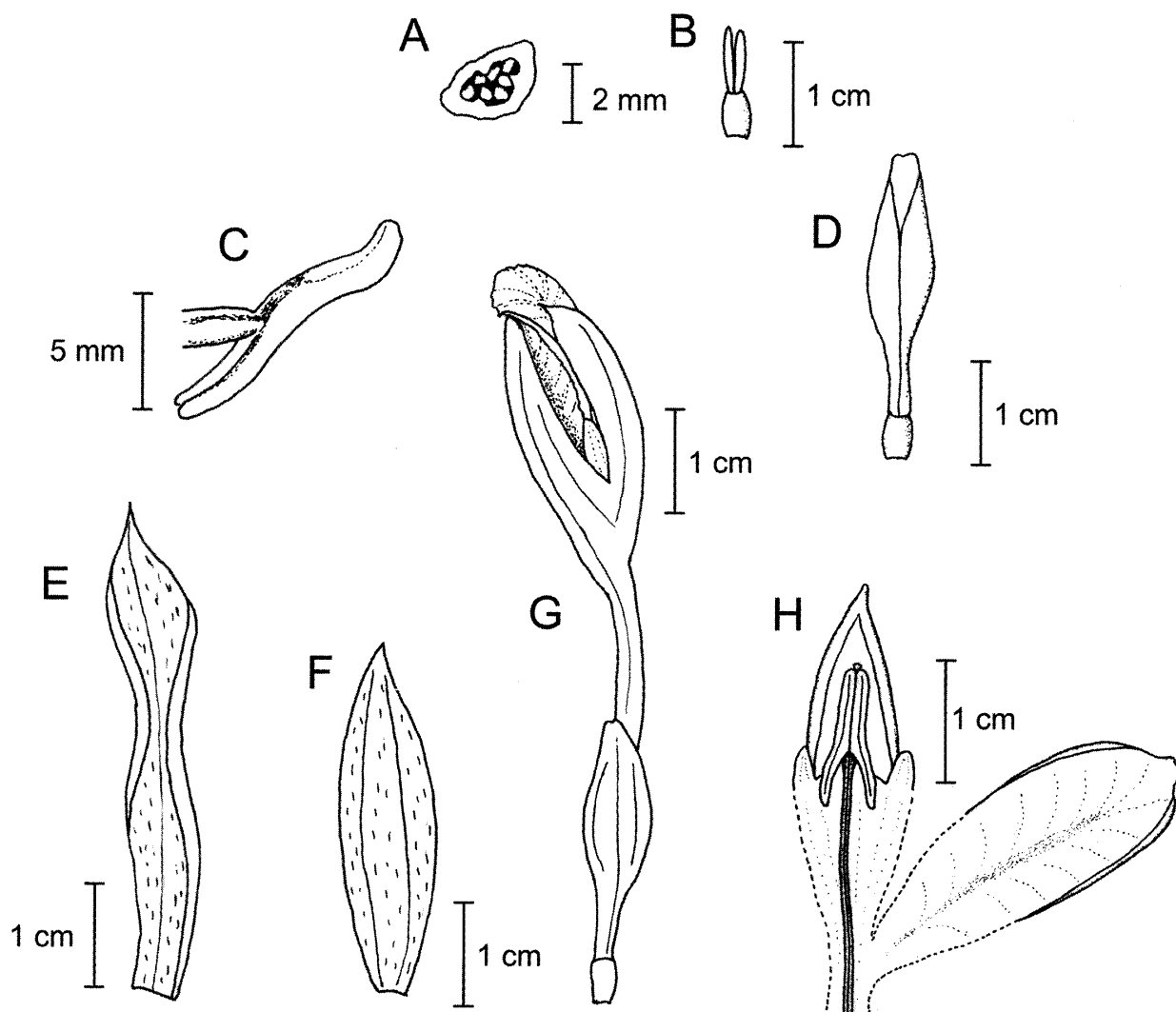


FIG. 1. *Myxochlamys mullerensis*. A: Cross section of ovary. B: Epigynous gland. C: Anther. D: Calyx. E: Bract. F: Bracteole. G: Flower. H: Part of flower showing corolla tube with a furrow enclosing a style, lateral staminodes, dorsal corolla lobe, anther, and labelum (from spirit-fixed material of H. Okada *et al.* KT-671).

Distribution: West and Central Kalimantan.

Etymology: The highly viscous mucus from glands on the bracts is pooled in the axils of the imbricate bracts. The name of the new genus is derived from these features (*Myxo-* slimy + *chlamys-* covering, mantle).

Additional specimens examined. INDONESIA.

Central Kalimantan: Samba, 1994-1995, Cutting block of PT Handiyani (0°43'22.5"S, 112°50'37.5"E), *JK Jarvie* & *A Ruskandi* 5447 (BO); Near Muara Joloi (0°02'S 114°06'E), *CS Awmack* 109 (K), *ibidem*, *CS Awmack*

198 (K); *ibidem*, *CS Awmack* 199 (K). **West Kalimantan:** Serawai, 8 km northeast of Desa Jelundung, Batu Lintang (0°30'57.9"S, 112°36'7.1"E), *AC Church* & *UM Mahyar* 1702 (BO).

Molecular phylogenetic analyses using ITS and combined datasets

The ITS-1 had a total aligned length of 184 bp (unaligned sequences ranged from 173 to 217 bp) with a mean guanine-cytosine (GC) content of 53.5%, the 5.8S region had an aligned length of 164 bp (range, 158-164 bp) and a GC content of

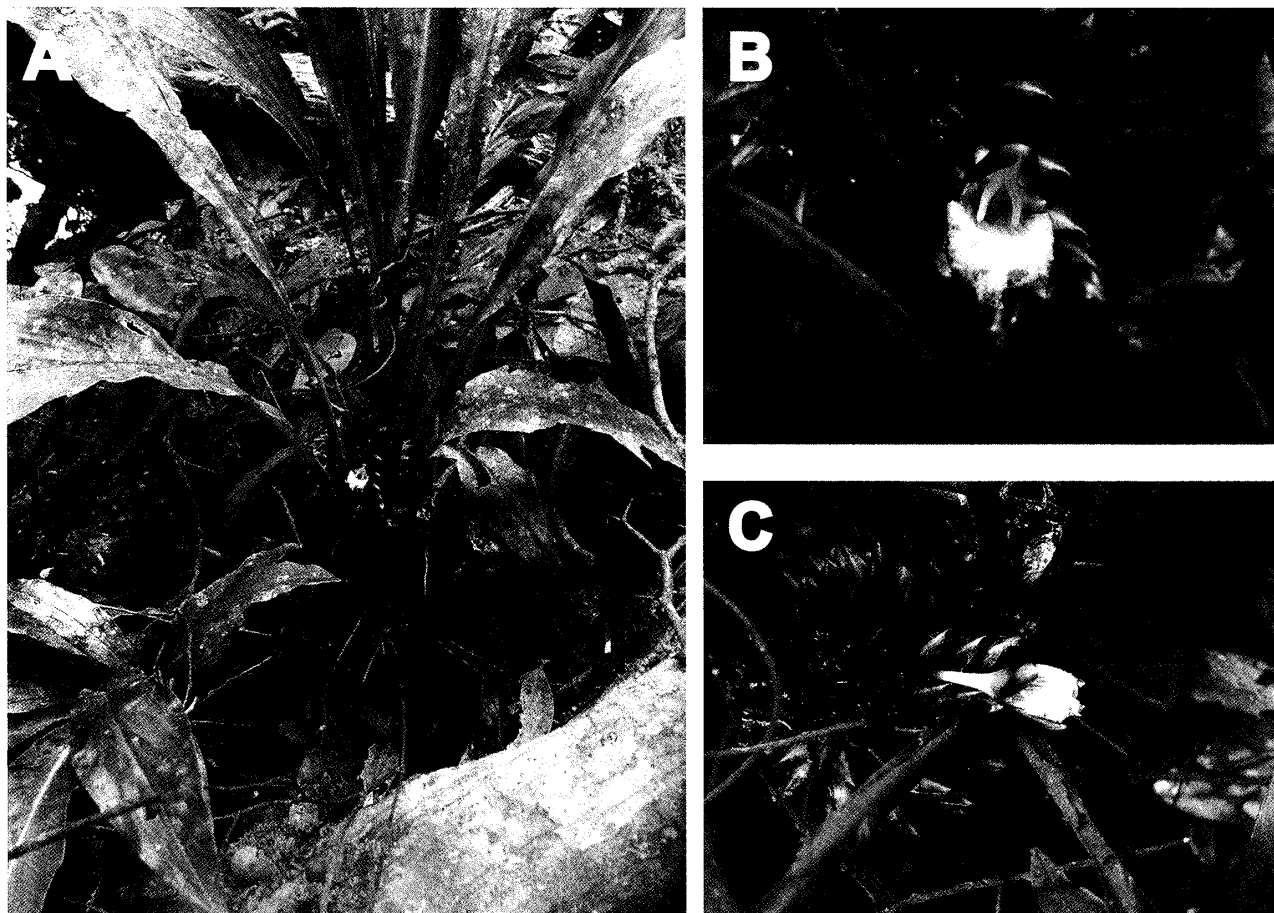


FIG. 2. *Myxochlamys mullerensis*. A: Habitat. B: Close-up of flower. C: Inflorescence (all photos by H. Okada.; H. Okada et al. KT-671).

51.7%, and the ITS-2 had an aligned length of 226 bp (range, 208–270 bp) with a GC content of 58.1%. In *Myxochlamys*, the ITS-1 sequence was 179 bp in length with a GC content of 52.5%, the 5.8S region was 164 bp in length with a GC content of 51.8%, and the ITS-2 region was 229 bp in length with a GC content of 59.8%.

Analysis of the ITS sequence data, excluding the ambiguously aligned regions by using 70 taxa, resulted in eight equally parsimonious trees of 1508 steps (number of parsimony-informative characters, 272; consistency index [CI] = 0.404; retention index [RI] = 0.622). In the strict consensus tree (Fig. 3), *Myxochlamys* is found in the Zingiberoideae clade, which is sister to the *Scaphochlamys* and *Distichochlamys* clades, but bootstrap support for this relationship is low

(58.4%). The result of Bayesian inference of phylogeny (posterior probabilities: PP), however, strongly supported (PP = 100) this relationship (Fig. 4).

Congruence of the data partitions (chloroplast and nuclear) could not be rejected by the ILD test ($p = 0.98$). Analysis of a combined matrix containing 2227 characters for 47 taxa resulted in 1617 equally parsimonious trees of 1711 steps (number of parsimony-informative characters, 401; consistency index [CI] = 0.527; retention index [RI] = 0.603). The strict consensus tree is shown in Fig. 5. Both MP and Bayesian analyses (Fig. 6) yielded trees of similar topology, but the Bayesian tree was more resolved in the Zingiberoideae clade. *Myxochlamys* is sister to *Scaphochlamys* (BS/PP = 74.3/100), and *Distichochlamys* is sister to these genera (BS/PP = 72.9/100) (Figs. 5, 6).

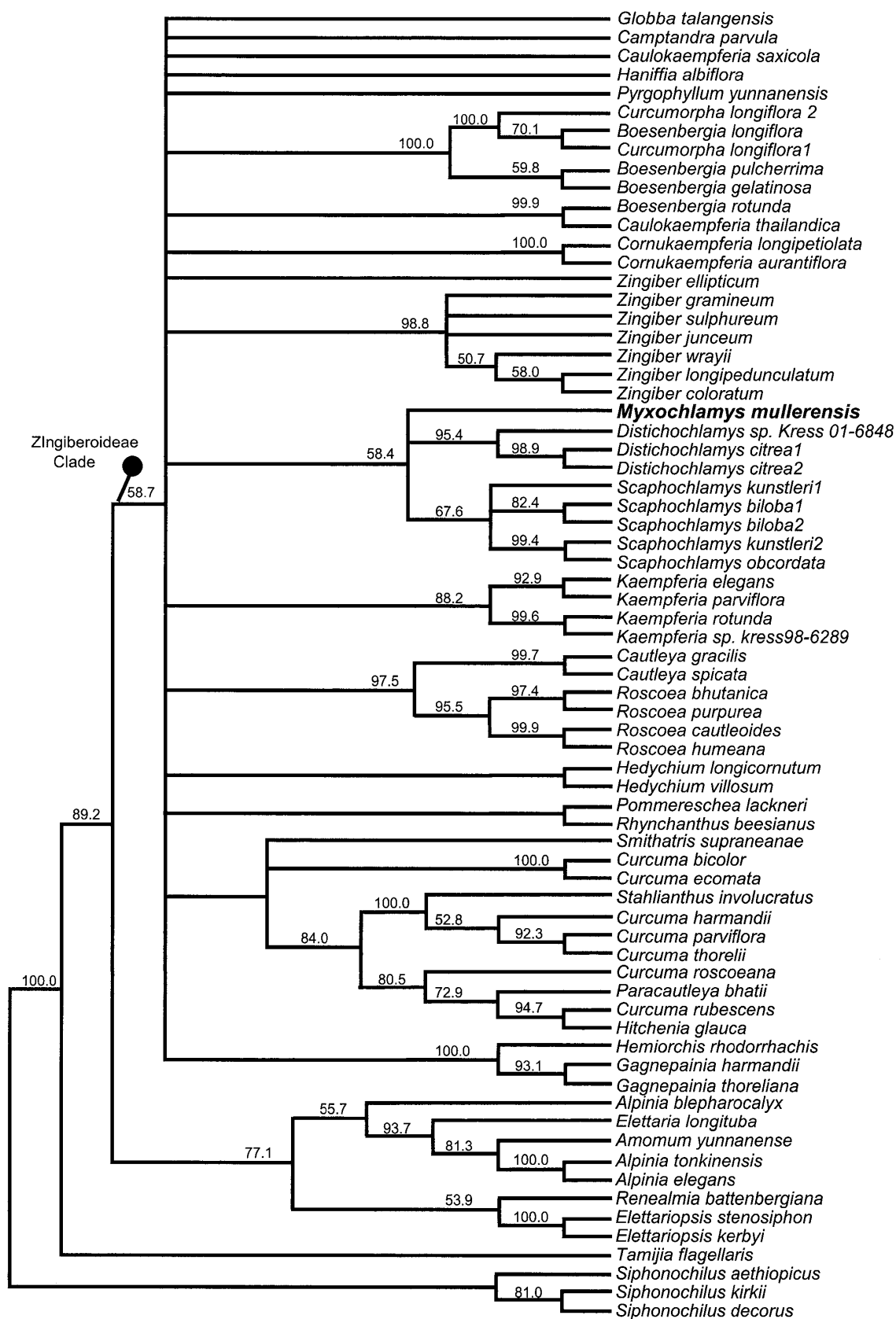


FIG. 3. Strict consensus of eight maximum parsimonious trees of the subfamily Zingiberoideae resulting from analysis of the ITS sequence data (length = 1508, consistency index = 0.404, and retention index = 0.622). Numbers above branches indicate bootstrap values (>50%).

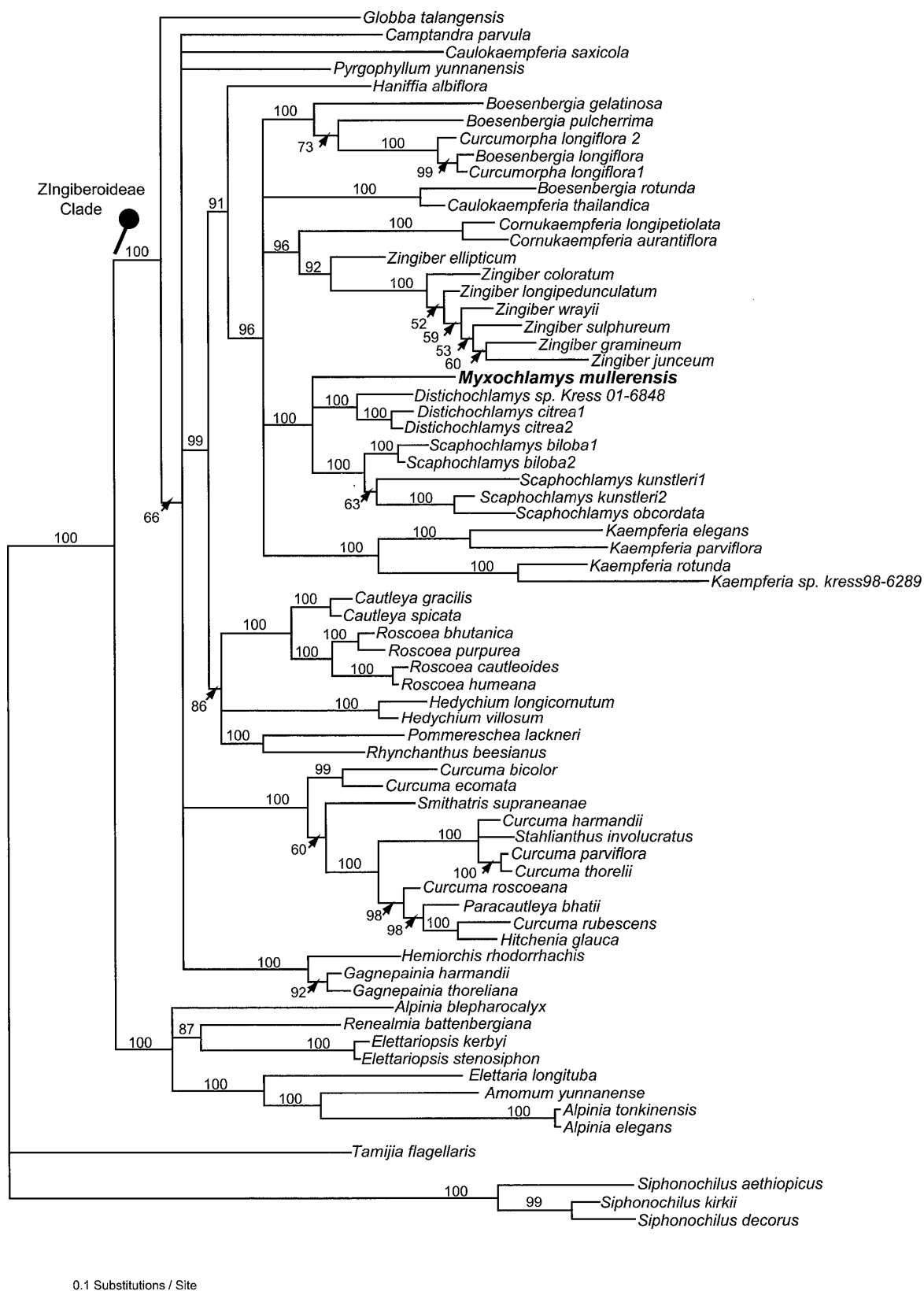


FIG. 4. Bayesian consensus phylogram based on branch length obtained from ITS sequence data. Numbers above branches indicate posterior probabilities (PP) higher than 50%.

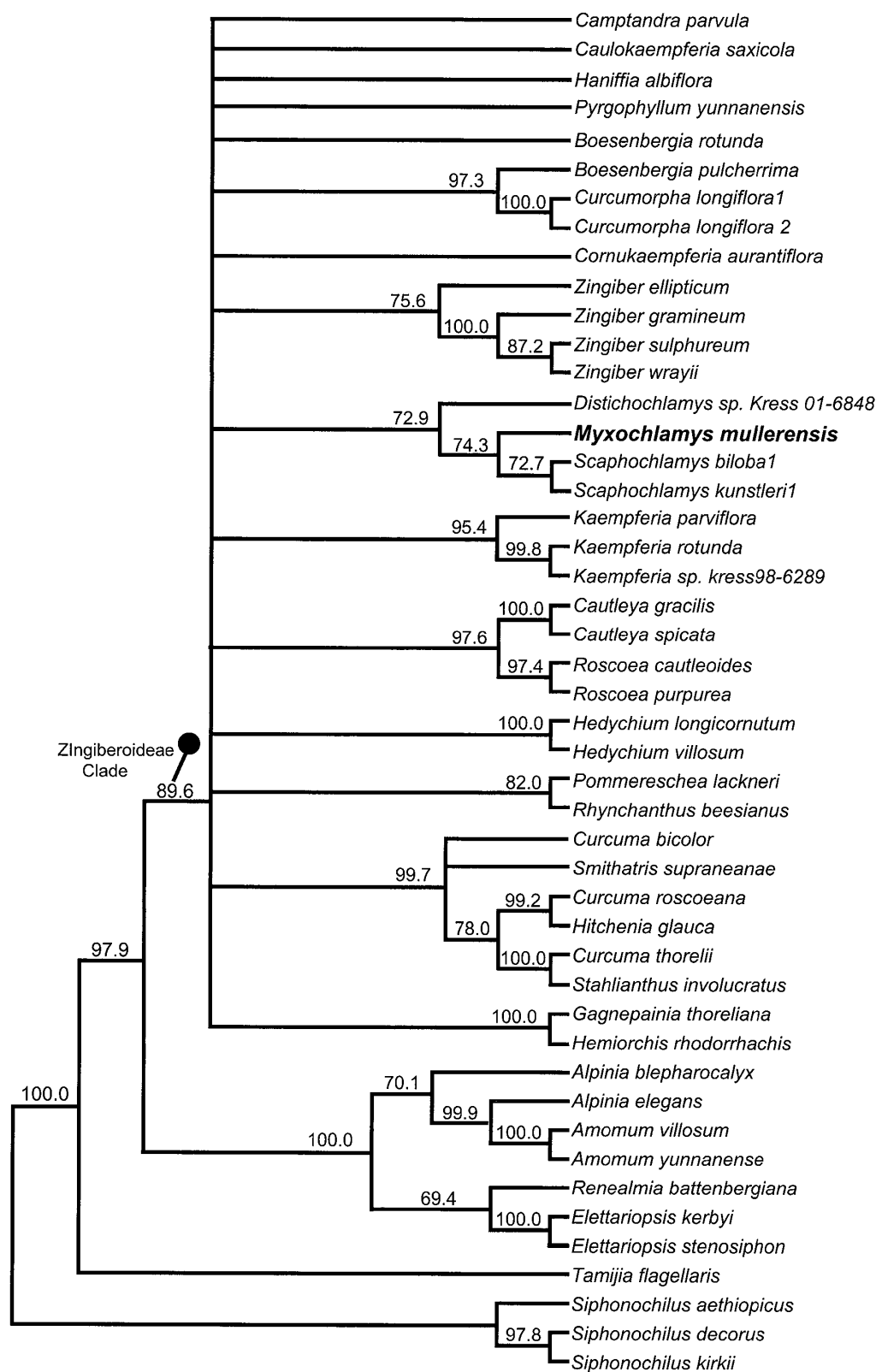


FIG. 5. Strict consensus of 1617 maximum parsimonious trees of subfamily Zingiberoideae resulting from analysis of combined ITS and *matK* region sequence data (length = 1711, consistency index = 0.527, and retention index = 0.603). Numbers above branches indicate bootstrap values (>50%).

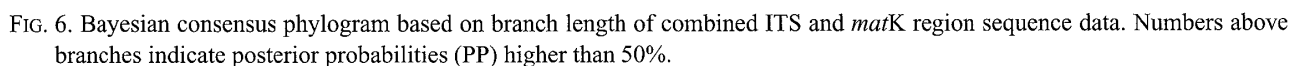


TABLE 1. Comparison of key characters between *Myxochlamys* and related genera

	Arrangement of bracts	Mode of flowering	Flowers	1st bracteole	Corolla tube	Thecae	Anther	Ovary
<i>Myxochlamys mullerensis</i>	Spiral	Base-apex (indeterminate)	Solitary	Open to base, Opposite bract; keels 2	with a groove formed by the inner surface	Basal spurs	Versatile	Unilocular with basal placentation
<i>Scaphochlamys</i>	Spiral	Base-apex (indeterminate)	Usually in cincinni	Open to base, Opposite bract, often more or less keeled (2 keels only in <i>S.</i> <i>calicicola</i>)	without such a groove	With very short, free, basal spurs (no spur in <i>S. calicicola</i>)	Adnate	Unilocular or trilocular with basal placentation
<i>Distichochlamys</i>	Distichous	Base-apex (indeterminate)	In cincinni	Tubular; keels 2	without such a groove	Spurs absent	Adnate	Trilocular

Discussion

Myxochlamys mullerensis is placed in the Zingiberoideae in the phylogenetic analyses based on the ITS and the combined ITS and *matK* region sequence data (BS/PP = 58.7/100 from ITS data, 89.6/100 from the combined data). In terms of morphology, *Myxochlamys mullerensis* could also be placed in the tribe Zingibereae, subfamily Zingiberoideae, in the classification system of Zingiberaceae by Kress *et al.* (2002) by virtue of the parallel orientation of the plane of distichy of its leafy shoots, its well-developed lateral staminodes, and labellum not connate to the filament. The unilocular ovary with basal placentation is rather rare in this tribe, however; a transition in the ovary type within some genera, e.g., *Boesenbergia*, *Haplochorema*, and *Scaphochlamys*, from trilocular with axile placentation to unilocular with free or basal placentation has been reported (Sakai & Nagamasu 2000).

Our molecular phylogenetic analyses suggest the affinity of *Myxochlamys* to *Distichochlamys* and *Scaphochlamys* (Figs. 3-6). *Myxochlamys* is sister to the *Distichochlamys* and *Scaphochlamys* clades as shown by the ITS data set analysis (Figs. 3-4), although the relationships among these three subclades are unresolved in both the MP and Bayesian trees. Further, both *Distichochlamys* and

Scaphochlamys are moderately supported subclades based on their species alone (*Scaphochlamys* subclade: BS/PP = 67.6/100; *Distichochlamys* subclade: BS/PP = 95.4/100), and *Myxochlamys* was placed outside of these genera. In the combined data set phylogeny, *Myxochlamys* was found to be sister to the *Scaphochlamys* clade (BS/PP = 74.3/100) and *Distichochlamys* was the sister of these two genera (BS/PP = 72.9/100). The results suggest that these three genera are closely related.

Morphologically, *Myxochlamys* is similar to *Scaphochlamys* in that it lacks a distinct pseudostem, but the spiral arrangement of bracts differs. At BO and K, most specimens of *Myxochlamys* without flowers were identified as *Scaphochlamys*, probably based on inflorescence and stem characteristics. There are also significant morphological differences, however, between *Myxochlamys* and *Scaphochlamys*. For example, flowers are borne singly in *Myxochlamys* vs. borne in cincinni; corolla tube with a groove enveloping the style inside vs. lacking such a groove; labellum concave vs. bilobed or entire, but never concave; anthers versatile vs. adnate. *Distichochlamys* is unique and distinct from *Myxochlamys* in that it has tubular bracteoles and distichously arranged bracts (Newman 1995). Furthermore, *Distichochlamys* has adnate anthers lacking spurs, produces flowers in cincinni, and

has a flat, bilobed labellum, while *Myxochlamys* has versatile anthers with long spurs, produces a single flower per bract, and has a concave, entire labellum. Comparison of key characters between *Myxochlamys* and the other genera is shown in Table 1. Among these characters, the versatile anthers are rather rare in the Zingiberaceae and are found only in five genera besides *Myxochlamys*: *Camptandra*, *Cautleya*, *Curcuma*, *Paracautleya*, and *Roscoea* (Larsen *et al.* 1998). The groove within the corolla tube is also uncommon and so far is known only in the monotypic *Stadiochilus* and a few species of *Hedychium* and *Zingiber* (Smith 1980).

Myxochlamys might be placed in *Scaphochlamys* as a peculiar species, but we hesitated to expand the circumscription of the latter genus because of poor support from molecular phylogenetic analyses and such significant morphological differences. Further study of *Myxochlamys* and related genera is required before firm conclusions on its placement can be reached.

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Appendix 1. Genbank accession numbers and voucher specimens used in this study.

Species	ITS	matK	References / Voucher
<i>Alpinia blepharocalyx</i> K. Schum.	AF478709	AF478809	Kress <i>et al.</i> 2002
<i>Alpinia elegans</i> K. Schum.	AF478713	AF478813	Kress <i>et al.</i> 2002
<i>Alpinia tonkinensis</i> Gagnep.	AY742386	-	Kress <i>et al.</i> 2005
<i>Amomum villosum</i> Lour.	AY769828	AF478824	Harris <i>et al.</i> 2005(ITS), Kress <i>et al.</i> 2002 (matK)
<i>Amomum yunnanense</i> S. Q. Tong	AY352012	AY352042	Xia <i>et al.</i> 2004
<i>Boesenbergia gelatinosa</i> K. Larsen	AY424744	-	Ngamriabsakul <i>et al.</i> 2003
<i>Boesenbergia longiflora</i> Kuntze	AY424745	-	Ngamriabsakul <i>et al.</i> 2003
<i>Boesenbergia pulcherrima</i> Kuntze	AF478725	AF478825	Kress <i>et al.</i> 2002
<i>Boesenbergia rotunda</i> (L.) Mansf.	AF478727	AF478826	Kress <i>et al.</i> 2002
<i>Camptandra parvula</i> Ridl.	AF478730	AF478830	Kress <i>et al.</i> 2002
<i>Caulokaempferia saxicola</i> K. Larsen	AY478732	AF478831	Kress <i>et al.</i> 2002
<i>Caulokaempferia thailandica</i> K. Larsen	AY424748	-	Ngamriabsakul <i>et al.</i> 2003
<i>Cautleya gracilis</i> (Sm.) Dandy	AF478734	AF478833	Kress <i>et al.</i> 2002
<i>Cautleya spicata</i> Baker	AF478735	AF478834	Kress <i>et al.</i> 2002
<i>Cornukaempferia aurantiflora</i> J. Mood & K. Larsen	AF478736	AF478835	Kress <i>et al.</i> 2002
<i>Cornukaempferia longipetiolata</i> J. Mood & K. Larsen	AY424750	-	Ngamriabsakul <i>et al.</i> 2003
<i>Curcuma bicolor</i> J. Mood & K. Larsen	AF478737	AF478837	Kress <i>et al.</i> 2002
<i>Curcuma ecomata</i> Craib	AY424753	-	Ngamriabsakul <i>et al.</i> 2003
<i>Curcuma harmandii</i> Gagnep.	AY424754	-	Ngamriabsakul <i>et al.</i> 2003
<i>Curcuma parviflora</i> Wall.	AY424755	-	Ngamriabsakul <i>et al.</i> 2003
<i>Curcuma roscoeana</i> Wall.	AF478739	AB047741	Kress <i>et al.</i> 2002 (ITS) / Cao <i>et al.</i> unpublished (matK)
<i>Curcuma rubescens</i> Roxb.	AY424756	-	Ngamriabsakul <i>et al.</i> 2003
<i>Curcuma thorelii</i> Gagnep.	AF478741	AF478841	Kress <i>et al.</i> 2002
<i>Curcumorpha longiflora</i> (Wall.) A. S. Rao & D. M. Verma 1	AF478742	AF478842	Kress <i>et al.</i> 2002
<i>Curcumorpha longiflora</i> (Wall.) A. S. Rao & D. M. Verma 2	AF478743	AF478843	Kress <i>et al.</i> 2002
<i>Distichochlamys citrea</i> M. F. Newman 1	AF478744	-	Kress <i>et al.</i> 2002
<i>Distichochlamys citrea</i> M. F. Newman 2	AY424757	-	Ngamriabsakul <i>et al.</i> 2003
<i>Distichochlamys</i> sp. Kress 01-6848	AF478745	AF478844	Kress <i>et al.</i> 2002
<i>Elettaria longituba</i> (Ridl.) Holttum	AB097228	-	Sakai <i>et al.</i> unpublished
<i>Elettariopsis kerbyi</i> R. M. Sm.	AF414496	AF478845	Pedersen 2004 (ITS) / Kress <i>et al.</i> 2002 (matK)
<i>Elettariopsis stenosphon</i> (K. Schum.) B. L. Burt & R. M. Sm.	AF478748	AF478847	Kress <i>et al.</i> 2002
<i>Gagnepainia harmandii</i> K. Schum.	AY339740	-	Williams <i>et al.</i> 2004
<i>Gagnepainia thoreliana</i> K. Schum.	AF478752	AF478851	Kress <i>et al.</i> 2002
<i>Globba talangensis</i> A. Takano et H. Okada	AY339735	-	Williams <i>et al.</i> 2004
<i>Haniffia albiflora</i> K. Larsen & J. Mood	AF478756	AF478855	Kress <i>et al.</i> 2002
<i>Hedychium longicornutum</i> Griff. ex Baker	AF478761	AF478860	Kress <i>et al.</i> 2002
<i>Hedychium villosum</i> Wall.	AF478762	AF478861	Kress <i>et al.</i> 2002
<i>Hemiorchis rhodorrhachis</i> K. Schum.	AY339706	AY341090	Williams <i>et al.</i> 2004
<i>Hitchenia glauca</i> Wall.	AF478765	AF478864	Kress <i>et al.</i> 2002
<i>Kaempferia elegans</i> Wall.	AY424764	-	Ngamriabsakul <i>et al.</i> 2003
<i>Kaempferia parviflora</i> Wall.	AJ388292	AB232052	Searle & Hedderson 2000
<i>Kaempferia rotunda</i> L.	AF478767	AF478868	Kress <i>et al.</i> 2002
<i>Kaempferia</i> sp. kress98-6289	AF478768	AF478869	Kress <i>et al.</i> 2002
<i>Myxochlamys mullerensis</i> A. Takano & Nagam.	AB245522	AB269791	This study: H. Okada <i>et al.</i> KT-671
<i>Paracautleya bhatii</i> R. M. Sm.	AY424766	-	Ngamriabsakul <i>et al.</i> 2003
<i>Pommereschea lackneri</i> Wittm.	AF478776	AF478877	Kress <i>et al.</i> 2002
<i>Pyrgophyllum yunnanensis</i> T. L. Wu & Z. Y. Chen	AF478777	AF478878	Kress <i>et al.</i> 2002
<i>Renealmia battenbergiana</i> Cummins ex Baker	AF478779	AF478880	Kress <i>et al.</i> 2002
<i>Rhynchanthus beesianus</i> W. W. Sm.	AF478784	AF478885	Kress <i>et al.</i> 2002
<i>Roscoea bhutanica</i> C. Ngamriabsakul	AY424768	-	Ngamriabsakul <i>et al.</i> 2003
<i>Roscoea cautleoides</i> Gagnep.	AF478736	AF478887	Kress <i>et al.</i> 2002
<i>Roscoea humeana</i> Balf.f. & W. W. Sm.	AF202406	-	Wood <i>et al.</i> 2000
<i>Roscoea purpurea</i> Sm.	AF478787	AF478888	Kress <i>et al.</i> 2002
<i>Scaphochlamys biloba</i> (Ridl.) Holttum	AF478788	AY478889	Kress <i>et al.</i> 2002
<i>Scaphochlamys biloba</i> (Ridl.) Holttum2	AF202416	-	Wood <i>et al.</i> 2000
<i>Scaphochlamys kunstleri</i> (Baker) Holttum	AF478789	AY478890	Kress <i>et al.</i> 2002

Appendix 1. continued.

Species	ITS	<i>matK</i>	References / Voucher
<i>Scaphochlamys kunstleri</i> (Baker) Holttum	AJ388287	-	Searle & Hedderson 2000
<i>Scaphochlamys obcordata</i> P. Sirirugsa & K. Larsen	AJ388286	-	Searle & Hedderson 2000
<i>Siphonochilus aethiopicus</i> (Schweinf.) B. L. Burt	AF478792	AF478893	Kress <i>et al.</i> 2002
<i>Siphonochilus decorus</i> (Druten) Lock	AF478793	AF478894	Kress <i>et al.</i> 2002
<i>Siphonochilus kirkii</i> (Hook.) B. L. Burt	AF478794	AF478895	Kress <i>et al.</i> 2002
<i>Smithatris supraneaanae</i> W. J. Kress & K. Larsen	AF478795	AF478896	Kress <i>et al.</i> 2002
<i>Stahlianthus involucratus</i> (King ex Baker) R. M. Sm.	AF478796	AF478897	Kress <i>et al.</i> 2002
<i>Tamijia flagellaris</i> S. Sakai & Nagam.	AF478797	AF478898	Kress <i>et al.</i> 2002
<i>Zingiber coloratum</i> N. E. Br.	AF414498	-	Pedersen 2004 (ITS)
<i>Zinigber ellipticum</i> (S. Q. Tong & Y. M. Xia) S. Q. Tong & Y. M. Xia	AF478799	AF478901	Kress <i>et al.</i> 2002
<i>Zingiber gramineum</i> Noronha	AF478800	AB088799	Kress <i>et al.</i> 2002 (ITS) / Tamura <i>et al.</i> 2004 (<i>matK</i>)
<i>Zingiber junceum</i> Gagnep.	AY424774	-	Ngamriabsakul <i>et al.</i> 2003
<i>Zingiber longipedunculatum</i> Ridl.	AB097254	-	Sakai <i>et al.</i> unpublished
<i>Zingiber sulphureum</i> Burkill ex I. Theilade	AF478801	AF478904	Kress <i>et al.</i> 2002
<i>Zingiber wrayii</i> Prain ex Ridl.	AF478802	AF478905	Kress <i>et al.</i> 2002